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- 1 -

SEQUENCE LISTING

<110> THE CORPORATION OF THE TRUSTEES OF THE ORDER OF THE SISTERS OF
MERCY IN QUEENSLAND

<120> NOVEL THERAPEUTIC MOLECULES AND USES THEREOF

<130> 12381870/TDO

<150> 2002953223

<151> 2002-06-12

<160> 32

<170> PatentIn version 3.1

<210> 1

<211> 5622

<212> DNA

<213> mammalian

<220>

<221> CDS

<222> (1)..(5619)

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Val Glu Gly Thr Leu Cys Lys	Thr Ala Ile Pro Tyr	Lys Arg Lys	
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Tyr Leu Ser Asp Asn His Ile	Leu Ile Ser Ala Leu	Val Ile Ala	
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<213> mammalian

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<222> (45)..(740)
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Ala Leu Pro Ala Leu Leu Leu Pro Leu Leu Gly Leu Ala Ala Ala Ala
5          10          15          20

gtc gcg gac tgt cct tca tct act tgg att cag ttc caa gac agt tgt 152
Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe Gln Asp Ser Cys
25          30          35

tac att ttt ctc caa gaa gcc atc aaa gta gaa agc ata gag gat gtc 200
Tyr Ile Phe Leu Gln Glu Ala Ile Lys Val Glu Ser Ile Glu Asp Val
40          45          50

aga aat cag tgt act gac cat gga gcg gac atg ata agc ata cat aat 248
Arg Asn Gln Cys Thr Asp His Gly Ala Asp Met Ile Ser Ile His Asn
55          60          65

gaa gaa gaa aat gct ttt ata ctg gat act ttg aaa aag caa tgg aaa 296

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[illegible]

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<213> mammalian

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<400> 5

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1          5          10          15

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```

Ala Ala Ala Ala Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
          20          25          30

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Gln Asp Ser Cys Tyr Ile Phe Leu Gln Glu Ala Ile Lys Val Glu Ser
          35          40          45

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```

Ile Glu Asp Val Arg Asn Gln Cys Thr Asp His Gly Ala Asp Met Ile
          50          55          60

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```

Ser Ile His Asn Glu Glu Glu Asn Ala Phe Ile Leu Asp Thr Leu Lys
65          70          75          80

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Lys Gln Trp Lys Gly Pro Asp Asp Ile Leu Leu Gly Met Phe Tyr Asp
85 90 95

Thr Asp Asp Ala Ser Phe Lys Trp Phe Asp Asn Ser Asn Met Thr Phe
100 105 110

Asp Lys Trp Thr Asp Gln Asp Asp Glu Asp Leu Val Asp Thr Cys
115 120 125

Ala Phe Leu His Ile Lys Thr Gly Glu Trp Lys Lys Gly Asn Cys Glu
130 135 140

Val Ser Ser Val Glu Gly Thr Leu Cys Lys Thr Ala Ile Pro Tyr Lys
145 150 155 160

Arg Lys Tyr Leu Ser Asp Asn His Ile Leu Ile Ser Ala Leu Val Ile
165 170 175

Ala Ser Thr Val Ile Leu Thr Val Leu Gly Ala Ile Ile Trp Phe Leu
180 185 190

Tyr Lys Lys His Ser Asp Ser Arg Phe Thr Thr Val Phe Ser Thr Ala
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3740

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gtc atg ccc cac gca gcg ctg tcc tcg ctc gtg ctg ctg agc ctc gcc 408
Met Pro His Ala Ala Leu Ser Ser Leu Val Leu Leu Ser Leu Ala
1 5 10 15
act gcc atc gtc gcc gac tgt cct tca tct acc tgg gtc cag ttc caa 456
Thr Ala Ile Val Ala Asp Cys Pro Ser Ser Thr Trp Val Gln Phe Gln
20 25 30
ggc agc tgt tat gct ttt ctt caa gta acc atc aat gtg gaa aac ata 504
Gly Ser Cys Tyr Ala Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile
35 40 45
gag gat gtc aga aaa cag tgc act gac cac ggg gca gac atg gta agc 552
Glu Asp Val Arg Lys Gln Cys Thr Asp His Gly Ala Asp Met Val Ser
50 55 60
ata cac aat gaa gag gaa aac gcg ttt ata ctg gac act ttg caa aag 600
Ile His Asn Glu Glu Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys
65 70 75
cga tgg aag ggt cca gat gat ctc ctg cta ggc atg ttc tat gac act 648
Arg Trp Lys Gly Pro Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr
80 85 90 95
gat gat gca act ttc aag tgg tat gat cat tca aat atg aca ttc gac 696
Asp Asp Ala Thr Phe Lys Trp Tyr Asp His Ser Asn Met Thr Phe Asp
100 105 110

aag tgg gca gat caa gat ggt gag gac cta gtt gat acc tgt ggt ttt	744
Lys Trp Ala Asp Gln Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe	
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ctg tac acc aag aca ggt gaa tgg aga aaa ggg gat tgt gaa atc tct	792
Leu Tyr Thr Lys Thr Gly Glu Trp Arg Lys Gly Asp Cys Glu Ile Ser	
130 135 140	
tct gtg gag gga aca ctt tgc aaa gca gca atc cca tat gac aag aag	840
Ser Val Glu Gly Thr Leu Cys Lys Ala Ala Ile Pro Tyr Asp Lys Lys	
145 150 155	
tat tta tca gat aac cac att tta ata tcg act ctg gtg atc gct agc	888
Tyr Leu Ser Asp Asn His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser	
160 165 170 175	
aca gta act ctg gca gtt ttg gga gcg atc att tgg ttc ctc tat aga	936
Thr Val Thr Leu Ala Val Leu Gly Ala Ile Ile Trp Phe Leu Tyr Arg	
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aga aac gcg cgc tct ggc ttc acc tct ttt tca cct gca cca ctg tca	984
Arg Asn Ala Arg Ser Gly Phe Thr Ser Phe Ser Pro Ala Pro Leu Ser	
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cct tac agt gat ggc tgt gcc ctg gta gtt gca gaa gaa gat gaa tat	1032
Pro Tyr Ser Asp Gly Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr	
210 215 220	
gct gtt cag ctg gac taagagtttg gtaatatcag gccagcatat tgartccatt	1087
Ala Val Gln Leu Asp	
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20 25 30

Ser Cys Tyr Ala Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile Glu
35 40 45

Asp Val Arg Lys Gln Cys Thr Asp His Gly Ala Asp Met Val Ser Ile
50 55 60

His Asn Glu Glu Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys Arg
65 70 75 80

Trp Lys Gly Pro Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr Asp
85 90 95

Asp Ala Thr Phe Lys Trp Tyr Asp His Ser Asn Met Thr Phe Asp Lys
100 105 110

Trp Ala Asp Gln Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe Leu
115 120 125

Tyr Thr Lys Thr Gly Glu Trp Arg Lys Gly Asp Cys Glu Ile Ser Ser
130 135 140

Val Glu Gly Thr Leu Cys Lys Ala Ala Ile Pro Tyr Asp Lys Lys Tyr
145 150 155 160

Leu Ser Asp Asn His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr
165 170 175

Val Thr Leu Ala Val Leu Gly Ala Ile Ile Trp Phe Leu Tyr Arg Arg
180 185 190

Asn Ala Arg Ser Gly Phe Thr Ser Phe Ser Pro Ala Pro Leu Ser Pro
195 200 205

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210 215 220

Val Gln Leu Asp
225

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ccttcaagat aaataaaaac gttgtaaaat ctttcagact ctaatgaagt caagtttact 180

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gac tgt cct tcg tcc atc tgg gtt cag ttc caa ggc agc tgt tac act 96
Asp Cys Pro Ser Ser Ile Trp Val Gln Phe Gln Gly Ser Cys Tyr Thr
20 25 30

ttt ctt caa gta acc atc aat gtg gaa aac ata gag gat gtc aga aag 144
Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile Glu Asp Val Arg Lys
35 40 45

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cag tgt act gat cac ggg gca gac ctg gta agt ata cac aat gaa gaa	192
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Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys Arg Trp Lys Gly Pro	
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gat gat ctt ctg cta ggc atg ttt tat gac act gat gat gca agt ttc	288
Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr Asp Asp Ala Ser Phe	
85 90 95	
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Lys Trp Phe Asp Gln Ser Asn Met Thr Phe Asp Lys Trp Ala Asp Glu	
100 105 110	
gat ggt gag gac cta gtt gac acc tgt ggt ttt ctg tat gcc aag aca	384
Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe Leu Tyr Ala Lys Thr	
115 120 125	
ggt gaa tgg aga aaa gga aat tgt gaa atg tct tct gtg acr gga aca	432
Gly Glu Trp Arg Lys Gly Asn Cys Glu Met Ser Ser Val Xaa Gly Thr	
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ctt tgc aaa aca gca atc cca tat gac aag aag tat tta tca gat aac	480
Leu Cys Lys Thr Ala Ile Pro Tyr Asp Lys Lys Tyr Leu Ser Asp Asn	
145 150 155 160	
cac att tta ata tcg act ctg gtg atc gct agc aca gtg act ctg gca	528
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165 170 175	
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Val Leu Gly Ala Val Ile Trp Phe Leu Tyr Arg Arg Ser Ala Arg Ser	
180 185 190	
ggc ttc acc tct ttc tct cct gca cca caa tca cct tac agt gat ggc	624
Gly Phe Thr Ser Phe Ser Pro Ala Pro Gln Ser Pro Tyr Ser Asp Gly	
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Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr Ser Val Gln Leu Asp	
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aaaaaaaa	979

<210> 11
 <211> 224
 <212> PRT
 <213> mammalian

<220>
 <221> misc_feature
 <222> (5)..(5)
 <223> The 'Xaa' at location 5 stands for Leu.

<220>
 <221> misc_feature
 <222> (13)..(13)
 <223> The 'Xaa' at location 13 stands for Ala, or Val.

<220>
 <221> misc_feature
 <222> (142)..(142)
 <223> The 'Xaa' at location 142 stands for Thr.

<400> 11

His Glu Ala Ser Xaa Val Leu Leu Ser Leu Ala Thr Xaa Ile Phe Ala
 1 5 10 15

Asp Cys Pro Ser Ser Ile Trp Val Gln Phe Gln Gly Ser Cys Tyr Thr
 20 25 30

Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile Glu Asp Val Arg Lys
 35 40 45

Gln Cys Thr Asp His Gly Ala Asp Leu Val Ser Ile His Asn Glu Glu
 50 55 60

Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys Arg Trp Lys Gly Pro
 65 70 75 80

Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr Asp Asp Ala Ser Phe
 85 90 95

Lys Trp Phe Asp Gln Ser Asn Met Thr Phe Asp Lys Trp Ala Asp Glu
 100 105 110

Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe Leu Tyr Ala Lys Thr
 115 120 125

Gly Glu Trp Arg Lys Gly Asn Cys Glu Met Ser Ser Val Xaa Gly Thr
 130 135 140

Leu Cys Lys Thr Ala Ile Pro Tyr Asp Lys Lys Tyr Leu Ser Asp Asn
145 150 155 160

His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr Val Thr Leu Ala
165 170 175

Val Leu Gly Ala Val Ile Trp Phe Leu Tyr Arg Arg Ser Ala Arg Ser
180 185 190

Gly Phe Thr Ser Phe Ser Pro Ala Pro Gln Ser Pro Tyr Ser Asp Gly
195 200 205

Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr Ser Val Gln Leu Asp
210 215 220

<210> 12
<211> 979
<212> DNA
<213> mammalian

<400> 12
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cttttgtatc tcctacagtc tttcgtcaca tgactagtgc cccgtctgga ccattcatat 180
gtgttacttc ttcttttgcg taaatatgac ctgtgaaatg ttttcgctac ctttccgggc 240
ctactagaag acgatccgta caaaatactg tgactactac gttcaaagtt caccaaacta 300
gtcagtttat actgtaagct gttcacccgt ctactcctac cactcctgga tcaactgtgg 360
acacccaaaag acatacgggt ctgtccactt acctcttttc ctttaacact ttacagaaga 420
cactgycctt gtgaaacggt ttgtcgtag ggtatactgt tcttcataaa tagtctattg 480
gtgtaaaatt atagctgaga ccactagcga tcgtgtcact gagaccgtca aaaccctcgc 540
cagtaaacca aggagatatc ttcctcgcgt gcgagaccga agtggagaaa gagaggacgt 600
gggtgttagtg gaatgtcact accgacacga gaccatcaac gccttcttct acttatgaga 660
caagtcgacc tgactctcaa acccttgtag tctgctcgtg tgacttgtgg aactgttctt 720
tattaaagga tacgttctaa cagtacattt taaacgggtgc cttttgactt ggaaaatacc 780
ataaggaata agaagattgt tataaaagta cataagttac actgttttgt atttggaaga 840
ctaattttcc tttttttcat ccaaagtctt ttccttgatc gtgtctcgat tgaatgtcca 900

aaagaattca tcaaaagtaa actcatttac ttctgatgtc atgttatttc gaccattttg 960
cgtttttttt tttttttttt 979

<210> 13
<211> 483
<212> DNA
<213> mammalian

<220>
<221> misc_feature
<222> (43)..(43)
<223> n is any nucleic acid

<400> 13
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atatttatca gataaccgca ttttaatatc agctttgggtg attgctagca cagtaattct 180
gacagttctg ggagcagttg tttggttctt gtacaaaaga agtttggatt ctggtttcac 240
cacagttttt tcagctgcac accaatcacc ttataatgat gactgtgttt tagtagttgc 300
agaggaaaac gaatatgata ttcaatttaa ctaagatttt ggaaatatca gactaagaca 360
aatacctttc agtgattcct ctgtaagatt tcaatataaa acctgataat gaaatttagt 420
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atg 483

<210> 14
<211> 27
<212> DNA
<213> mammalian

<220>
<221> CDS
<222> (1)..(27)
<223>

<400> 14
aaa gtg cct ctg ggc cct gat tac aca 27
Lys Val Pro Leu Gly Pro Asp Tyr Thr
1 5

<210> 15
<211> 9
<212> PRT
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<400> 15

Lys Val Pro Leu Gly Pro Asp Tyr Thr
1 5

<210> 16
<211> 42
<212> DNA
<213> mammalian

<220>
<221> CDS
<222> (1)..(42)
<223>

<400> 16

aaa gtg cct ctg gac tgt cct tca tct act tgg att cag ttc 42
Lys Val Pro Leu Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
1 5 10

<210> 17
<211> 14
<212> PRT
<213> mammalian

<400> 17

Lys Val Pro Leu Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
1 5 10

<210> 18
<211> 42
<212> DNA
<213> mammalian

<220>
<221> CDS
<222> (1)..(42)
<223>

<400> 18

gct gcc gtc gcg gac tgt cct tca tct act tgg att cag ttc 42
Ala Ala Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
1 5 10

<210> 19
 <211> 14
 <212> PRT
 <213> mammalian

<400> 19

Ala Ala Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
 1 5 10

<210> 20
 <211> 5454
 <212> DNA
 <213> mammalian

<220>
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 <222> (1)..(5451)
 <223>

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 Met Arg Thr Gly Trp Ala Thr Pro Arg Arg Pro Ala Gly Leu Leu Met
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 ctg ctc ttc tgg ttc ttc gat ctc gcg gag ccc tct ggc cgc gca gct 96
 Leu Leu Phe Trp Phe Phe Asp Leu Ala Glu Pro Ser Gly Arg Ala Ala
 20 25 30
 aat gac ccc ttc acc atc gtc cat gga aat acg ggc aag tgc atc aag 144
 Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys
 35 40 45
 cca gtg tat ggc tgg ata gta gca gac gac tgt gat gaa act gag gac 192
 Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp
 50 55 60
 aag tta tgg aag tgg gtg tcc cag cat cgg ctc ttt cat ttg cac tcc 240
 Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser
 65 70 75 80
 caa aag tgc ctt ggc ctc gat att acc aaa tcg gta aat gag ctg aga 288
 Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg
 85 90 95
 atg ttc agc tgt gac tcc agt gcc atg ctg tgg tgg aaa tgt gag cac 336
 Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His
 100 105 110
 cac tct ctg tac gga gct gcc cgg tac cgg ctg gct ctg aag gat gga 384
 His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly
 115 120 125

cat ggc aca gca atc tca aat gca tct gat gtc tgg aag aaa gga ggc His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly 130 135 140	432
tca gag gaa agc ctt tgt gac cag cct tat cat gag atc tat acc aga Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg 145 150 155 160	480
gat ggg aac tct tat ggg aga cct tgt gaa ttt cca ttc tta att gat Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp 165 170 175	528
ggg acc tgg cat cat gat tgc att ctt gat gaa gat cat agt ggg cca Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro 180 185 190	576
tgg tgt gcc acc acc tta aat tat gaa tat gac cga aag tgg ggc atc Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile 195 200 205	624
tgc tta aag cct gaa aac ggt tgt gaa gat aat tgg gaa aag aac gag Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu 210 215 220	672
cag ttt gga agt tgc tac caa ttt aat act cag acg gct ctt tct tgg Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp 225 230 235 240	720
aaa gaa gct tat gtt tca tgt cag aat caa gga gct gat tta ctg agc Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser 245 250 255	768
atc aac agt gct gct gaa tta act tac ctt aaa gaa aaa gaa ggc att Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile 260 265 270	816
gct aag att ttc tgg att ggt tta aat cag cta tac tct gct aga ggc Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly 275 280 285	864
tgg gaa tgg tca gac cac aaa cca tta aac ttt ctc aac tgg gat cca Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro 290 295 300	912
gac agg ccc agt gca cct act ata ggt ggc tcc agc tgt gca aga atg Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met 305 310 315 320	960
gat gct gag tct ggt ctg tgg cag agc ttt tcc tgt gaa gct caa ctg Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu 325 330 335	1008
ccc tat gtc tgc agg aaa cca tta aat aat aca gtg gag tta aca gat Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp 340 345 350	1056

gtc tgg aca tac tca gat acc cgc tgt gat gca ggc tgg ctg cca aat	1104
Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn	
355 360 365	
aat gga ttt tgc tat ctg ctg gta aat gaa agt aat tcc tgg gat aag	1152
Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys	
370 375 380	
gca cat gcg aaa tgc aaa gcc ttc agt agt gac cta atc agc att cat	1200
Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His	
385 390 395 400	
tct cta gca gat gtg gag gtg gtt gtc aca aaa ctc cat aat gag gat	1248
Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp	
405 410 415	
atc aaa gaa gaa gtg tgg ata ggc ctt aag aac ata aac ata cca act	1296
Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr	
420 425 430	
tta ttt cag tgg tca gat ggt act gaa gtt act cta aca tat tgg gat	1344
Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp	
435 440 445	
gag aat gag cca aat gtt ccc tac aat aag acg ccc aac tgt gtt tcc	1392
Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser	
450 455 460	
tac tta gga gag cta ggt cag tgg aaa gtc caa tca tgt gag gag aaa	1440
Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys	
465 470 475 480	
cta aaa tat gta tgc aag aga aag gga gaa aaa ctg aat gac gca agt	1488
Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser	
485 490 495	
tct gat aag atg tgt cct cca gat gag ggc tgg aag aga cat gga gaa	1536
Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu	
500 505 510	
acc tgt tac aag att tat gag gat gag gtc cct ttt gga aca aac tgc	1584
Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys	
515 520 525	
aat ctg act atc act agc aga ttt gag caa gaa tac cta aat gat ttg	1632
Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu	
530 535 540	
atg aaa aag tat gat aaa tct cta aga aaa tac ttc tgg act ggc ctg	1680
Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu	
545 550 555 560	
aga gat gta gat tct tgt gga gag tat aac tgg gca act gtt ggt gga	1728
Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly	
565 570 575	

aga	agg	cgg	gct	gta	acc	ttt	tcc	aac	tgg	aat	ttt	ctt	gag	cca	gct	1776
Arg	Arg	Arg	Ala	Val	Thr	Phe	Ser	Asn	Trp	Asn	Phe	Leu	Glu	Pro	Ala	
			580					585					590			
tcc	ccg	ggc	ggc	tgc	gtg	gct	atg	tct	act	gga	aag	tct	gtt	gga	aag	1824
Ser	Pro	Gly	Gly	Cys	Val	Ala	Met	Ser	Thr	Gly	Lys	Ser	Val	Gly	Lys	
		595					600					605				
tgg	gag	gtg	aag	gac	tgc	aga	agc	ttc	aaa	gca	ctt	tca	att	tgc	aag	1872
Trp	Glu	Val	Lys	Asp	Cys	Arg	Ser	Phe	Lys	Ala	Leu	Ser	Ile	Cys	Lys	
	610					615					620					
aaa	atg	agt	gga	ccc	ctt	ggg	cct	gaa	gaa	gca	tcc	cct	aag	cct	gat	1920
Lys	Met	Ser	Gly	Pro	Leu	Gly	Pro	Glu	Glu	Ala	Ser	Pro	Lys	Pro	Asp	
625					630					635					640	
gac	ccc	tgt	cct	gaa	ggc	tgg	cag	agt	ttc	ccc	gca	agt	ctt	tct	tgt	1968
Asp	Pro	Cys	Pro	Glu	Gly	Trp	Gln	Ser	Phe	Pro	Ala	Ser	Leu	Ser	Cys	
				645					650					655		
tat	aag	gta	ttc	cat	gca	gaa	aga	att	gta	aga	aag	agg	aac	tgg	gaa	2016
Tyr	Lys	Val	Phe	His	Ala	Glu	Arg	Ile	Val	Arg	Lys	Arg	Asn	Trp	Glu	
			660					665					670			
gaa	gct	gaa	cga	ttc	tgc	caa	gcc	ctt	gga	gca	cac	ctt	tct	agc	ttc	2064
Glu	Ala	Glu	Arg	Phe	Cys	Gln	Ala	Leu	Gly	Ala	His	Leu	Ser	Ser	Phe	
		675					680					685				
agc	cat	gtg	gat	gaa	ata	aag	gaa	ttt	ctt	cac	ttt	tta	acg	gac	cag	2112
Ser	His	Val	Asp	Glu	Ile	Lys	Glu	Phe	Leu	His	Phe	Leu	Thr	Asp	Gln	
	690					695					700					
ttc	agt	ggc	cag	cat	tgg	ctg	tgg	att	ggg	ttg	aat	aaa	agg	agc	cca	2160
Phe	Ser	Gly	Gln	His	Trp	Leu	Trp	Ile	Gly	Leu	Asn	Lys	Arg	Ser	Pro	
705					710					715					720	
gat	tta	caa	gga	tcc	tgg	caa	tgg	agt	gat	cgt	aca	cca	gtg	tct	act	2208
Asp	Leu	Gln	Gly	Ser	Trp	Gln	Trp	Ser	Asp	Arg	Thr	Pro	Val	Ser	Thr	
				725					730					735		
att	atc	atg	cca	aat	gag	ttt	cag	cag	gat	tat	gac	atc	aga	gac	tgt	2256
Ile	Ile	Met	Pro	Asn	Glu	Phe	Gln	Gln	Asp	Tyr	Asp	Ile	Arg	Asp	Cys	
			740					745					750			
gct	gct	gtc	aag	gta	ttt	cat	agg	cca	tgg	cga	aga	ggc	tgg	cat	ttc	2304
Ala	Ala	Val	Lys	Val	Phe	His	Arg	Pro	Trp	Arg	Arg	Gly	Trp	His	Phe	
		755					760					765				
tat	gat	gat	aga	gaa	ttt	att	tat	ttg	agg	cct	ttt	gct	tgt	gat	aca	2352
Tyr	Asp	Asp	Arg	Glu	Phe	Ile	Tyr	Leu	Arg	Pro	Phe	Ala	Cys	Asp	Thr	
	770					775					780					
aaa	ctt	gaa	tgg	gtg	tgc	caa	att	cca	aaa	ggc	cgt	act	cca	aaa	aca	2400
Lys	Leu	Glu	Trp	Val	Cys	Gln	Ile	Pro	Lys	Gly	Arg	Thr	Pro	Lys	Thr	
785					790					795					800	

cca gac tgg tac aat cca gac cgt gct gga att cat gga cct cca ctt	2448
Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu	
805 810 815	
ata att gaa gga agt gaa tat tgg ttt gtt gct gat ctt cac cta aac	2496
Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn	
820 825 830	
tat gaa gaa gcc gtc ctg tac tgt gcc agc aat cac agc ttt ctt gcg	2544
Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala	
835 840 845	
act ata aca tct ttt gtg gga cta aaa gcc atc aaa aac aaa ata gca	2592
Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala	
850 855 860	
aat ata tct ggt gat gga cag aag tgg tgg ata aga att agc gag tgg	2640
Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp	
865 870 875 880	
cca ata gat gat cat ttt aca tac tca cga tat cca tgg cac cgc ttt	2688
Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe	
885 890 895	
cct gtg aca ttt gga gag gaa tgc ttg tac atg tct gcc aag act tgg	2736
Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp	
900 905 910	
ctt atc gac tta ggt aaa cca aca gac tgt agt acc aag ttg ccc ttc	2784
Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe	
915 920 925	
atc tgt gaa aaa tat aat gtt tct tcg tta gag aaa tac agc cca gat	2832
Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp	
930 935 940	
tct gca gct aaa gtg caa tgt tct gag caa tgg att cct ttt cag aat	2880
Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn	
945 950 955 960	
aag tgt ttt cta aag atc aaa ccc gtg tct ctc aca ttt tct caa gca	2928
Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala	
965 970 975	
agc gat acc tgt cac tcc tat ggt ggc acc ctt cct tca gtg ttg agc	2976
Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser	
980 985 990	
cag att gaa caa gac ttt att aca tcc ttg ctt ccg gat atg gaa gct	3024
Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala	
995 1000 1005	
act tta tgg att ggt ttg cgc tgg act gcc tat gaa aag ata aac	3069
Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn	
1010 1015 1020	

aaa tgg aca gat aac aga gag ctg acg tac agt aac ttt cac cca	3114
Lys Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro	
1025 1030 1035	
tta ttg gtt agt ggg agg ctg aga ata cca gaa aat ttt ttt gag	3159
Leu Leu Val Ser Gly Arg Leu Arg Ile Pro Glu Asn Phe Phe Glu	
1040 1045 1050	
gaa gag tct cgc tac cac tgt gcc cta ata ctc aac ctc caa aaa	3204
Glu Glu Ser Arg Tyr His Cys Ala Leu Ile Leu Asn Leu Gln Lys	
1055 1060 1065	
tca ccg ttt act ggg acg tgg aat ttt aca tcc tgc agt gaa cgc	3249
Ser Pro Phe Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg	
1070 1075 1080	
cac ttt gtg tct ctc tgt cag aaa tat tca gaa gtt aaa agc aga	3294
His Phe Val Ser Leu Cys Gln Lys Tyr Ser Glu Val Lys Ser Arg	
1085 1090 1095	
cag acg ttg cag aat gct tca gaa act gta aag tat cta aat aat	3339
Gln Thr Leu Gln Asn Ala Ser Glu Thr Val Lys Tyr Leu Asn Asn	
1100 1105 1110	
ctg tac aaa ata atc cca aag act ctg act tgg cac agt gct aaa	3384
Leu Tyr Lys Ile Ile Pro Lys Thr Leu Thr Trp His Ser Ala Lys	
1115 1120 1125	
agg gag tgt ctg aaa agt aac atg cag ctg gtg agc atc acg gac	3429
Arg Glu Cys Leu Lys Ser Asn Met Gln Leu Val Ser Ile Thr Asp	
1130 1135 1140	
cct tac cag cag gca ttc ctc agt gtg cag gcg ctc ctt cac aac	3474
Pro Tyr Gln Gln Ala Phe Leu Ser Val Gln Ala Leu Leu His Asn	
1145 1150 1155	
tct tcc tta tgg atc gga ctc ttc agt caa gat gat gaa ctc aac	3519
Ser Ser Leu Trp Ile Gly Leu Phe Ser Gln Asp Asp Glu Leu Asn	
1160 1165 1170	
ttt ggt tgg tca gat ggg aaa cgt ctt cat ttt agt cgc tgg gct	3564
Phe Gly Trp Ser Asp Gly Lys Arg Leu His Phe Ser Arg Trp Ala	
1175 1180 1185	
gaa act aat ggg caa ctc gaa gac tgt gta gta tta gac act gat	3609
Glu Thr Asn Gly Gln Leu Glu Asp Cys Val Val Leu Asp Thr Asp	
1190 1195 1200	
gga ttc tgg aaa aca gtt gat tgc aat gac aat caa cca ggt gct	3654
Gly Phe Trp Lys Thr Val Asp Cys Asn Asp Asn Gln Pro Gly Ala	
1205 1210 1215	
att tgc tac tat tca gga aat gag act gaa aaa gag gtc aaa cca	3699
Ile Cys Tyr Tyr Ser Gly Asn Glu Thr Glu Lys Glu Val Lys Pro	
1220 1225 1230	

gtt gac agt gtt aaa tgt cca tct cct gtt cta aat act ccg tgg	3744
Val Asp Ser Val Lys Cys Pro Ser Pro Val Leu Asn Thr Pro Trp	
1235 1240 1245	
ata cca ttt cag aac tgt tgc tac aat ttc ata ata aca aag aat	3789
Ile Pro Phe Gln Asn Cys Cys Tyr Asn Phe Ile Ile Thr Lys Asn	
1250 1255 1260	
agg cat atg gca aca aca cag gat gaa gtt cat act aaa tgc cag	3834
Arg His Met Ala Thr Thr Gln Asp Glu Val His Thr Lys Cys Gln	
1265 1270 1275	
aaa ctg aat cca aaa tca cat att ctg agt att cga gat gaa aag	3879
Lys Leu Asn Pro Lys Ser His Ile Leu Ser Ile Arg Asp Glu Lys	
1280 1285 1290	
gag aat aac ttt gtt ctt gag caa ctg ctg tac ttc aat tat atg	3924
Glu Asn Asn Phe Val Leu Glu Gln Leu Leu Tyr Phe Asn Tyr Met	
1295 1300 1305	
gct tca tgg gtc atg tta gga ata act tat aga aat aat tct ctt	3969
Ala Ser Trp Val Met Leu Gly Ile Thr Tyr Arg Asn Asn Ser Leu	
1310 1315 1320	
atg tgg ttt gat aag acc cca ctg tca tat aca cat tgg aga gca	4014
Met Trp Phe Asp Lys Thr Pro Leu Ser Tyr Thr His Trp Arg Ala	
1325 1330 1335	
gga aga cca act ata aaa aat gag aag ttt ttg gct ggt tta agt	4059
Gly Arg Pro Thr Ile Lys Asn Glu Lys Phe Leu Ala Gly Leu Ser	
1340 1345 1350	
act gac ggc ttc tgg gat att caa acc ttt aaa gtt att gaa gaa	4104
Thr Asp Gly Phe Trp Asp Ile Gln Thr Phe Lys Val Ile Glu Glu	
1355 1360 1365	
gca gtt tat ttt cac cag cac agc att ctt gct tgt aaa att gaa	4149
Ala Val Tyr Phe His Gln His Ser Ile Leu Ala Cys Lys Ile Glu	
1370 1375 1380	
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Met Val Asp Tyr Lys Glu Glu His Asn Thr Thr Leu Pro Gln Phe	
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Thr Trp Tyr Glu Ala Leu Asn Met Cys Ser Gln Ser Gly Gly His	
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His Asp	Gly Ser	Glu Ser	Ser Phe	Glu Trp	Ser Asp	Gly Ser	Thr	
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Val Leu	Leu Asp	Pro Lys	Gly Thr	Trp Lys	His Glu	Lys Cys	Asn	
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Ser Val	Lys Asp	Gly Ala	Ile Cys	Tyr Lys	Pro Thr	Lys Ser	Lys	
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Lys Leu	Ser Arg	Leu Thr	Tyr Ser	Ser Arg	Cys Pro	Ala Ala	Lys	
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Ser Asp	Gln Ala	Leu His	Ser Phe	Ser Glu	Ala Lys	Lys Leu	Cys	
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Ser Lys	His Asp	His Ser	Ala Thr	Ile Val	Ser Ile	Lys Asp	Glu	
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Asp Glu	Asn Lys	Phe Val	Ser Arg	Leu Met	Arg Glu	Asn Asn	Asn	
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Ile Thr	Met Arg	Val Trp	Leu Gly	Leu Ser	Gln His	Ser Val	Asp	
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Cys Pro	Ser Ser	Thr Trp	Ile Gln	Phe Gln	Asp Ser	Cys Tyr	Ile	
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Asn Gln	Cys Thr	Asp His	Gly Ala	Asp Met	Ile Ser	Ile His	Asn	
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Lys Gly Pro Asp Asp Ile Leu Leu Gly Met Phe Tyr Asp Thr Asp	
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Lys Trp Thr Asp Gln Asp Asp Asp Glu Asp Leu Val Asp Thr Cys	
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Tyr Lys Arg Lys Tyr Leu Ser Asp Asn His Ile Leu Ile Ser Ala	
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Ile Trp Phe Leu Tyr Lys Lys His Ser Asp Ser Arg Phe Thr Thr	
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35 40 45

Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp
50 55 60

Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser
65 70 75 80

Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg
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Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His
100 105 110

His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly
115 120 125

His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly
130 135 140

Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg
145 150 155 160

Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp
165 170 175

Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro
180 185 190

Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile
195 200 205

Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu
210 215 220

Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp
225 230 235 240

Lys	Glu	Ala	Tyr	Val	Ser	Cys	Gln	Asn	Gln	Gly	Ala	Asp	Leu	Leu	Ser	245	250	255
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Ala	Lys	Ile	Phe	Trp	Ile	Gly	Leu	Asn	Gln	Leu	Tyr	Ser	Ala	Arg	Gly	275	280	285
Trp	Glu	Trp	Ser	Asp	His	Lys	Pro	Leu	Asn	Phe	Leu	Asn	Trp	Asp	Pro	290	295	300
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Leu	Phe	Gln	Trp	Ser	Asp	Gly	Thr	Glu	Val	Thr	Leu	Thr	Tyr	Trp	Asp	435	440	445
Glu	Asn	Glu	Pro	Asn	Val	Pro	Tyr	Asn	Lys	Thr	Pro	Asn	Cys	Val	Ser	450	455	460

Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys
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485 490 495

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Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys
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Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu
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Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe
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Ser	His	Val	Asp	Glu	Ile	Lys	Glu	Phe	Leu	His	Phe	Leu	Thr	Asp	Gln	690	695	700
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Asp	Leu	Gln	Gly	Ser	Trp	Gln	Trp	Ser	Asp	Arg	Thr	Pro	Val	Ser	Thr	725	730	735
Ile	Ile	Met	Pro	Asn	Glu	Phe	Gln	Gln	Asp	Tyr	Asp	Ile	Arg	Asp	Cys	740	745	750
Ala	Ala	Val	Lys	Val	Phe	His	Arg	Pro	Trp	Arg	Arg	Gly	Trp	His	Phe	755	760	765
Tyr	Asp	Asp	Arg	Glu	Phe	Ile	Tyr	Leu	Arg	Pro	Phe	Ala	Cys	Asp	Thr	770	775	780
Lys	Leu	Glu	Trp	Val	Cys	Gln	Ile	Pro	Lys	Gly	Arg	Thr	Pro	Lys	Thr	785	790	795
Pro	Asp	Trp	Tyr	Asn	Pro	Asp	Arg	Ala	Gly	Ile	His	Gly	Pro	Pro	Leu	805	810	815
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Tyr	Glu	Glu	Ala	Val	Leu	Tyr	Cys	Ala	Ser	Asn	His	Ser	Phe	Leu	Ala	835	840	845
Thr	Ile	Thr	Ser	Phe	Val	Gly	Leu	Lys	Ala	Ile	Lys	Asn	Lys	Ile	Ala	850	855	860
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Pro	Ile	Asp	Asp	His	Phe	Thr	Tyr	Ser	Arg	Tyr	Pro	Trp	His	Arg	Phe	885	890	895
Pro	Val	Thr	Phe	Gly	Glu	Glu	Cys	Leu	Tyr	Met	Ser	Ala	Lys	Thr	Trp	900	905	910

Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe
915 920 925

Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp
930 935 940

Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn
945 950 955 960

Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala
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Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser
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Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala
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Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn
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